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097D61
ID 097D61 PRELIMINARY; PRT; 217 AA.
AC 097D61;
DT 01-OCT-2001 (T-EMBLrel. 18, Created)
DT 01-OCT-2001 (T-EMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Amino acid ABC transporter, permease component.
GN CAC3619.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Brelton G., Ometchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hiltl J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucet-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RA "Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum."
J. Bacteriol. 183:4823-4838(2001).
RL EMBL; AB007858; AAK81542.1; -.
DR InterPro; IPR000515; BPD_transp.
DR Pfam; PF00528; BPD_transp.1.
DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBERS.1.
KW Complete proteome.
SQ SEQUENCE 217 AA; 23743 MW; 36738BCDCDE8A2F CRC64;

Query Match 9.2%; Score 88.5; DB 16; Length 217;
Best Local Similarity 24.8%; Pred. No. 0.25;
Matches 55; Conservative 25; Mismatches 77; Indels 65; Gaps 10;

QY 16 SLHACIPCOLRCSSTPPLTCORVCNAY-----TNSYKGTNAI---LMTCLGI 62
DB 4 SSLNKYIPVLLDRTITLLTLCSSIIIGCTITIAMFKTSSVKVNLGKPYTWIRGT 63
QY 63 SLTISLAVFY--LMPFLRKISSEPLRDEF-----KNTGS-----GLGMANIDERS 108
DB 64 PLHLQIVYVYGGLPFSSDKLTMTMPKQALIGLSLNSGAVYAEIIRGILAIIDGQFEASK 123
QY 109 -----TCDEIILPRGLEVTVEEC-----TCEDCI-KSKPKVSDH 142
DB 124 ALGLTYGGMKRIITLQAIRVIVPCGNERTIAMIKDTSLVSVTIMELLARKQLLVSSSG 183
QY 143 CFFLPAMEGA--TIVTTKTNDYCSLPALASATIEKISIS 182
DB 184 DAVTPYLPFAGIFYLITLTITFTGIFSK-----IEKKLS 215

RESULT 3
ID 08R056 PRELIMINARY; PRT; 842 AA.
AC 08R056;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Hypothetical 94.5 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAUSBERG R.;
RA Strausberg R.;
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028286; AAH28286.1; -.
KW Hypothetical protein.
SQ SEQUENCE 842 AA; 94478 MW; 734C10D715E5BC92 CRC64;

Query Match 9.0%; Score 86.5; DB 11; Length 842;

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Best Local Similarity 22.7%; Pred. No. 1.9;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACIPCOLRCSSTPPLTCORVCNAYSTNSYKGTNAIIMTCLGLSLIISLAVPLMEL 77
DB 126 LVGCFCCMCRC-----CNK-CGEMHOKONAPRRRCGLSLIVLCLSLGLITY 176
QY 78 RKISEEPLKDEPKNTGSLGMANIDERSRTGD-EIIL---PRGLEVTVECTCE----- 129
DB 177 GVVANQQRTRIKRGOK-----LAKSNFRDQTLITPRKIDIVVEQYNTTKA 227
QY 130 ---DCIKS-----KPKVSDHCFPLPAMEGATILVTK-TNDYCKSLPAL- 172
DB 228 FSDLIGISVLCGRIKDQLEKPY-----TPVLEIRKAMATAIKOTDALQNMSSLSKS 280
QY 173 ---SATIEKISISA 183
DB 281 LQDAATQALNTNLSS 294

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RESULT 4
ID 09Y1X8 PRELIMINARY; PRT; 1193 AA.
AC 09Y1X8;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Protein tyrosine kinase.
GN EPTK178.
OS Ephydatia fluviatilis.
OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
OC Haplosclerida; Spongiaillidae; Ephydatia.
OX NCBI_TaxID=31330;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9246375; PubMed=10229568;
RA Suga H., Koyanagi M., Hoshiyama D., Ono K., Iwabe N., Kuma K.,
RA Miyata T.;
RA "Extensive gene duplication in the early evolution of animals before
the parazoan-eumetazoan split demonstrated by G proteins and protein
tyrosine kinases from sponge and hydra."
J. Mol. Evol. 48:646-653(1999).
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2160119; PubMed=11738833;
RA Suga H., Katoh K., Miyata T.;
RA "Sponge homologs of vertebrate protein tyrosine kinases and frequent
domain shufflings in the early evolution of animals before the
parazoan-eumetazoan split."
Gene 280:195-201(2001).
DR EMBL; AB006570; BAA81724.2; -.
DR HSSP; P08631; 1AD5.
DR InterPro; IPR000494; EGFR_L_domain.
DR InterPro; IPR000719; Euk_Pkinase.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001368; TNFR_c6.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR PRINTS; PR00109; TYRKINASE.
DR Prodom; PD000001; Euk_Pkinase; 2.
DR SMART; SM00261; FU; 6.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TYRKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
KW Kinase.
SQ SEQUENCE 1193 AA; 128169 MW; 009E4AC9BC12DF60 CRC64;

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Query Match      8.7% Score 85.5; DB 5; Length 1193;
Best Local Similarity 22.3%; Pred. No. 3.6;
Matches 37; Conservative 28; Mismatches 56; Indels 45; Gaps 8;

QY 2 LOMAGCCGQNFYDLDLACIPQRCGSSNTP-----LTCGRYCNASTVNSVKGTNAL 56
DB 715 LCVSGSCSNDTEYQDAALN-CLPCAGCIGCGSPSISQCLTCA--SGSCTTDDVOSSGII 771
QY 57 WTCLGLSLILSLA---VFVLMFLRKISSEPLKDEFKNTGSLGMANIDLEKSRGDEI 113
DB 772 GIVESIVIVPLATIVILFLVRYRHEKVKFKNTGTA--MCTSN-----GNET 820
QY 114 ILPRGLETVVECTCEDCIKSKPVSDH---CPLPAMEGATI 155
DB 821 LRP-----PKLPDATRLLITRPTALBGGQYL 847

RESULT 5
Q8RWV7 PRELIMINARY; PRT; 938 AA.
Q8RWV7
01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 103.6 kDa protein.
GN ATG48195.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carinici P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamuya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinzaki K.,
RA Davis R.W., Becker J.R., Theologis A.;
RT "Arabidopsis Full Length cDNA Clones."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY091078; AAM13898.1; -
KW Hypothetical protein.
SQ SEQUENCE 938 AA; 103602 MW; 3E78395D65D75C95 CRC64;

Query Match      8.7% Score 83.5; DB 10; Length 938;
Best Local Similarity 29.4%; Pred. No. 4.5;
Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps 9;

QY 38 QRYCNASTVNSVKGTNALMTCLGLSLISLAVFLMLRKISSEPLKD-EFKN--TGS 94
DB 29 ERYCSA---NSALGTPSW---C-----SSTGPRQDSFEFNFSIGP 62
QY 95 GLGMANIDLEKSRGDEIILPRGLETVVECTCEDCIKSKP-----KVSDHCPEPLAM 149
DB 63 SLVTLSSIDM--SRIGD-----RGHIFDEGSCNGRSSAPGLNTGNTVNDMCGDL--M 113
QY 150 EEGATI 155
DB 114 DGGATI 119

RESULT 6
Q9STR8 PRELIMINARY; PRT; 1998 AA.
Q9STR8
01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 13, Last annotation update)
DE Hypothetical 223.5 kDa protein.
SQ T24C20_80.

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OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Choiane N., Robert C., Brottier P., Wincker P., Catolico L.,
RA Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Rudd S.,
RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL096856; CAB51067.1; -
DR InterPro; IPR000515; BPD_transp.
DR InterPro; IPR001683; PX.
DR Pfam; PF00787; PX; 1.
DR SMART; SMO0312; PX; 1.
DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBER; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 1998 AA; 223513 MW; 8B3D6A03CD248F55 CRC64;

Query Match      8.7% Score 83.5; DB 10; Length 1998;
Best Local Similarity 29.4%; Pred. No. 11;
Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps 9;

QY 38 QRYCNASTVNSVKGTNALMTCLGLSLISLAVFLMLRKISSEPLKD-EFKN--TGS 94
DB 1089 ERYCSA---NSALGTPSW---C-----SSTGPRQDSFEFNFSIGP 1122
QY 95 GLGMANIDLEKSRGDEIILPRGLETVVECTCEDCIKSKP-----KVSDHCPEPLAM 149
DB 1123 SLVTLSSIDM--SRIGD-----RGHIFDEGSCNGRSSAPGLNTGNTVNDMCGDL--M 1173
QY 150 EEGATI 155
DB 1174 DGGATI 1179

RESULT 7
Q97491 PRELIMINARY; PRT; 327 AA.
Q97491
01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Fas protein.
GN FAS.
OS Ovis aries (sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Takagi M., Takahashi H., Kabeya H., Ohaishi K., Sugimoto C., Onuma M.;
RT "Cloning of sheep fas antigen."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011671; BAA37093.1; -
DR HSPB; P25445; IODP.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_C6; 3.
DR SMART; SMO0005; DEATH; 1.
DR SMART; SMO0208; TNFR; 3.
DR PROSITE; PS00117; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
DR PROSITE; PS00650; TNFR_NGFR_2; 2.
SQ SEQUENCE 327 AA; 36928 MW; SCFEE844B2BE387A CRC64;

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SQ SEQUENCE 595 AA; 65899 MW; 7858FC1A6560641 CRC64;  
 Query Match 8.4%; Score 81; DB 10; Length 595;  
 Best Local Similarity 24.5%; Pred. No. 4.9;  
 Matches 39; Conservative 27; Mismatches 49; Indels 44; Gaps 10;

QY 8 CSONEYFDSLHACIPQ--LRCSN-----TPPLTCOR-----YCN-----SV 45  
 DB 127 CRCEGFGDNFPLSAGCDVNECTTSSTIHRNCSDPKTCRKVGFGYCKGSGYRLDTT 186  
 QY 46 TNSVK-----GTNAIWTCLGLSLISLAVFVLMFLRKISSEPLKDE-FKRTSGGL-- 97  
 DB 187 TMSCKRKEFAWTTLLVTTTIGF-LVILLGVACIQGRMKHLKDTKLRBOFFBONGGMLTQ 245  
 QY 98 ---GMANID-----LEKSRG--DEIILPRGLETV 123  
 DB 246 RLSGPSNDVAKIFTEDEGKAKATNGVABSRILIGGSGGIV 284

TLT 11  
 92  
 AC 001892 PRELIMINARY; PRT; 773 AA.  
 DT 01-JUL-1997 (TREMBlrel. 04, Created)  
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE RO8F11.7 protein.  
 GN RO8F11.7  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_Taxid=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA MEDLINE=99069613; PubMed=9851916;  
 RX None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Mink P.;  
 RT "The sequence of C. elegans cosmid RO8F11."  
 RL Submitted (MAY-1997) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Waterston R.;  
 RT Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF003385; AAB54249.1; --  
 DR HSSP; P05164; ICP.  
 DR InterPro; IPR002007; Anim\_peroxidase.  
 DR Pfam; PF03098; An\_peroxidase; 1.  
 SQ SEQUENCE 773 AA; 83992 MW; 4E3373FDA4EC67C7 CRC64;

Query Match 8.4%; Score 81; DB 5; Length 773;  
 Best Local Similarity 21.7%; Pred. No. 6.6;  
 Matches 40; Conservative 25; Mismatches 91; Indels 28; Gaps 6;

QY 23 PCOLRCSNTPLTJCO-----RYCN-----ASVTSVKGNTALMTCL---GLSL 64  
 DB 184 PPKSNATQGGFPKSSDSDVHRIIRISITGVCNNRGKFTQANSTAIRRLTGTSYDGLQA 243  
 QY 65 IISLAVFLMFLRKISSEPLKDEFKNTG-SGLGMANIDLEKSGTGEIILPRGLETV 123  
 DB 244 IRNITSVTSPLPSTRLISNKLHDEGSTNPFSPVHLMQIGQFIADHIIIFPSSAKDG 303  
 QY 124 EECCEGDIKSKPKYDSDHCFPLPAMEGATILVTTKNDYCKSLPALSA-----TE 176  
 DB 304 SSLNCTSC--SSPTTISTNCAPIPAPADKRYFTVPSRTAECIRILTRALNQGSGFVRTQ 361

QY 177 IEKS 180  
 DB 362 IDON 365

RESULT 12  
 ID 081820 PRELIMINARY; PRT; 735 AA.  
 AC 081820;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Wall-associated kinase 1 (putative wall-associated kinase 1).  
 GN WAK1 OR P16F4.6  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_Taxid=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99308512; PubMed=10380805;  
 RA He Z.H., Cheeseman T., He D., Kohorn B.D.;  
 RT "A cluster of five cell wall associated receptor kinase genes, wak1-5,  
 RT are expressed in specific organs of Arabidopsis.";  
 RL Plant Mol. Biol. 39:1189-1196(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,  
 RA Dale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M.,  
 RA Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carninci P.,  
 RA Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,  
 RA Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,  
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,  
 RA Sakurai T., Satou M., Seki M., Shim P., Southwick A., Tracy S.E.,  
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;  
 RT "Full length cDNA of gene F16F4.6 (GI:8920634).";  
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 RN [1]  
 RP EMBL; AJ009696; CA08794.1; --  
 DR EMBL; AY039917; AA064021.1; --  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF CA.  
 DR InterPro; IPR000719; Euk\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR004040; STY\_kinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR SMART; SM00179; EGF CA; 1.  
 DR SMART; SM00001; EGF-like; 1.  
 DR SMART; SM00221; STYK; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS01187; EGF CA; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Calcium-binding; EGF-like domain; Glycoprotein; Kinase;  
 KW Repeat; Serine/threonine-protein kinase; Transferrase.  
 SQ SEQUENCE 735 AA; 81211 MW; AAD41A28296093B6 CRC64;

Query Match 8.3%; Score 80; DB 10; Length 735;  
 Best Local Similarity 24.2%; Pred. No. 8;  
 Matches 39; Conservative 27; Mismatches 49; Indels 46; Gaps 10;

QY 8 CSONEYFDSLHACIPQ--LRCSN-----TPPLTCOR-----YCN-----SV 45  
 DB 264 CRCEGFGDNFPLSAGCDVNECTTSSTIHRNCSDPKTCRKVGFGYCKGSGYRLDTT 323  
 QY 46 TNSVK-----GTNAIWTCLGLSLISLAVFVLMFLRKISSEPLKDE-FKRTSGGL-- 97  
 DB 324 TMSCKRKEFAWTTLLVTTTIGF-LVILLGVACIQGRMKHLKDTKLRBOFFBONGGMLTQ 382

QY 98 -----GMANID-----LEKRTG--DEILPRELEYTV 123  
 Db 383 RLSGAGPSNVVDYKIFTEDEMKATNGYASRLGGCGGCTV 423

## RESULT 13

Q26489 PRELIMINARY; PRT; 1299 AA.  
 AC Q26489;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Endoprotease furin.  
 GN FURIN.  
 OS Spodoptera frugiperda (Fall armyworm).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Noctuidae; Noctuidae; Amphipyritinae; Spodoptera.  
 NCBI\_TaxId=7108;  
 (1)

## SEQUENCE FROM N.A.

TISSUE=SF9;  
 RA Cieplik M., Kleink H.;  
 RT "Cloning and functional characterization of FURIN from Spodoptera  
 RT frugiperda (SF9) cells."  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z68888; CA93116.1; -.  
 DR HSPF; Q99405; 1MPF.  
 DR Interpro; IPR002174; Furin\_1like.  
 DR Interpro; IPR002029; Peptidase\_S8.  
 DR Interpro; IPR002884; P\_domain.  
 DR Pfam; PF01483; P; 1.  
 DR Pfam; PF00082; Peptidase\_S8; 1.  
 DR PRINTS; PR00723; SUBTILISIN.  
 DR ProDom; PD000717; P\_domain; 1.  
 DR SMART; SM00261; FU; 10.  
 DR PROSITE; PS00136; SUBTILASE ASP; 1.  
 DR PROSITE; PS00137; SUBTILASE HIS; 1.  
 DR PROSITE; PS00138; SUBTILASE\_SER; 1.  
 KW Protease.  
 SQ SEQUENCE 1299 AA; 142020 MW; 4C3799C7B8C572AB CRC64;

Query Match 8.2%; Score 79.5; DB 5; Length 1299;  
 Best Local Similarity 24.1%; Pred. No. 17;  
 Matches 39; Conservative 26; Mismatches 48; Indels 49; Gaps 11;

QY 8 CSQNEYFSLHACIPCOLRCS-----SNTPLTCQRYCNAS---VTVSVKGTNAIILW 57  
 1150 CSRPRLRIDRLNQCVCPC---CSEKRGVTNSTPTDC-CHCNPENGEICINSSVAGKRIAEW 1205  
 QY 56 TGLGIS-----LILSLAV-----FVLMFLRKISSEPLKDEFNKTSGLGGMAN 101  
 Db 1206 GMLHTRPSADAPSAVAVTIAACAAVGLFTVLVLVQHSPPREKTRKTSVRG----- 1259  
 QY 102 IDLEKSRGTDEILPR-GLGYVEECTCEDCIKSKPKVSDH 142  
 Db 1260 -VEYSR-----LPRTVDVFTV---LTSCTDQDESPVEYEH 1289

## RESULT 14

Q8VFMO PRELIMINARY; PRT; 314 AA.  
 AC Q8VFMO;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Olfactory receptor MOR202-16.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 (1)  
 RP SEQUENCE FROM N.A.

RA Zhang X., Firestein S.J.;  
 RT "The olfactory receptor gene superfamily of the mouse."  
 RL Nat. Neurosci. 0:0-0 (2002).  
 RN [2]

## SEQUENCE FROM N.A.

RA Adams M.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY073405; AAL61068.1; -.  
 DR Interpro; IPR00276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm3.1; 1.  
 DR PRINTS; PR00237; GPCR\_RHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECIP\_F1\_1; UNKNOWN\_1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECIP\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 314 AA; 34987 MW; DE5CDDF63E32F8D CRC64;

Query Match 8.1%; Score 78.5; DB 11; Length 314;  
 Best Local Similarity 30.4%; Pred. No. 4.4;  
 Matches 31; Conservative 15; Mismatches 41; Indels 15; Gaps 6;

QY 8 CSQNEYFSLHACIPCOLRCSNT-----PILTCQRYCNASVTVSVKGTNAIILMT 58  
 Db 146 CYMCGILOSSIHVAIAFLSCNSVNIHFCDIPPL-LDISCSDTYTNEL--TVLLIGT 202  
 QY 59 CLG-LSLIISLAVFLMP--LIRKISSEPLKDEFNKTSGLL 97  
 Db 203 CDGILTLVLINTVLIFLIFALIRMSVYEAQRKARSTCAASHLI 244

## RESULT 15

Q9H677 PRELIMINARY; PRT; 485 AA.  
 AC Q9H677;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE CDNA: FLJ22531 fls, clone HRC12890.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxId=9606;  
 (1)  
 RP SEQUENCE FROM N.A.  
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RA Okitani R., Oca T., Suuki Y., Odayashi M., Nishi T., Shibahara T.,  
 RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;  
 RT "NEO human cDNA sequencing project."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK026184; BAB15387.1; -.  
 SQ SEQUENCE 485 AA; 54051 MW; 4474E549ACD560C3 CRC64;

Query Match 8.1%; Score 78.5; DB 4; Length 485;  
 Best Local Similarity 26.3%; Pred. No. 7.2;  
 Matches 35; Conservative 17; Mismatches 48; Indels 33; Gaps 6;

QY 47 NSVKGTNAIILMTCLGLSLISLAVFLMFLRKISSEPLKDEFNKTS-----GLIGM 99  
 Db 185 NRISVSIFLXGPLPLILS-----TWGQMTTFPFDTSISLVDMKKYHLCMI 232  
 QY 100 ANIDLEKSRGTDEILPRGLGYVEECTCEDCIKSKPK-----VSDHCPPLPAME 150  
 Db 233 PNLDLNLDR--DVLTP-DVSQYVESSESDSQMTDQGTLLFLFVDFHSAPVQOME 288  
 QY 151 -EGATILVTTKTN 162  
 Db 289 IWGYVTLTLTHLN 301

Search completed: June 23, 2003, 08:39:06  
 Job time : 85.0818 secs